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4. de Preval et al. IMMUNOGENETICS (1987) 26(4-5): 249-257.
5. Irle et al. J. EXPERIMENTAL MEDICINE (1988 Mar 1) 167(3): 853-872.
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# Immunogenetics

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# Immunogenetics

Immunogenetics publishes original full length articles, brief communications, and reviews on research in the following areas: immunogenetics of cell interaction, immunogenetics of tissue differentiation and development, phylogeny of alloantigens and of immune response, genetic control of immune response and disease susceptibility, and genetics and biochemistry of alloantigens.

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Immunogenetics

## Assignm

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## Structural Comparison of the Genes of Two HLA-DR Supertypic Groups: The Loci Encoding DRw52 and DRw53 Are Not Truly Allelic

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**Abstract.** The organization and sequence of the *HLA-DR $\beta$*  chain genes are compared in the two supertypic groups, DRw52 and DRw53, which together account for more than 80% of *HLA-DR* alleles. From the structural data, we conclude that these two groups represent distinct lineages which have followed different patterns of evolution. The fine structure of the  $\beta$  chain locus encoding the DRw53 specificity corresponds most closely to the *DR $\beta$ II* pseudogene in the DRw52 haplotypes. Concomitantly, the *DR $\beta$ I* locus in DRw53 haplotypes is more closely related to both of the two expressed *DR $\beta$*  loci of the DRw52 haplotypes (*DR $\beta$ I* and *DR $\beta$ III*). These two loci are the result of a recent duplication. This leads to the proposal that both expressed *DR $\beta$*  chain genes in the DRw52 haplotypes (*DR $\beta$ I* and *DR $\beta$ III*) are derived from a single precursor locus, while the two loci expressed in the DRw53 haplotypes are derived from distinct ancestral loci. The genes encoding DRw52 and DRw53 are therefore not true alleles of the same original locus. A scheme is proposed that accounts for the evolution of DR specificities within the DRw52 and DRw53 groups of haplotypes. It is evident that the different *HLA-DR* alleles are not structurally equidistant and that one must take into consideration different degrees of heterozygosity or mismatch among the *DR* alleles.

### Introduction

A striking feature of the major histocompatibility complex (MHC) is its remarkable allelic polymorphism. This polymorphism is responsible for the phenomenon of restriction of antigen presentation to T lymphocytes of the same haplotype. The class II products of the MHC are involved in presentation of antigen to a subset of T lymphocytes. Different class II allelic products can present certain antigens with either low or high efficiency, thus determining

the extent of the immune response (reviewed by Benacerraf 1981, Nagy et al. 1981, Schwartz 1985). The biological significance of MHC class II polymorphism is the ability it confers to the population to cope with a variety of pathogens and thus to survive as a species.

The major class II product of the human MHC (*HLA*) is *HLA-DR*. This transmembrane protein is composed of two chains, the  $\alpha$  and  $\beta$  chains. The  $\alpha$  chain is encoded by a single locus (*A*) and shows no polymorphism. The  $\beta$  chains, on the contrary, are highly polymorphic and are encoded by several (*B*) loci (reviewed by Kaufman et al. 1984, Rollini et al. 1985). The correlation between the products of each of these individual  $\beta$  chain loci and the observed phenotypic traits such as serologic reactivity, alloreactive T-cell stimulation and restricted antigen presentation represents an important challenge.

*HLA-DR* was first defined by serology. Sera directed against *HLA-D/DR* molecules often recognize the products of several different alleles and are thus designated as supertypic sera. They define groups of cross-reactive haplotypes called "supertypic groups." Two major supertypic groups have been identified. The members of the DRw52 supertypic group, haplotypes *DR3*, *DR5*, *DRw6*, and *DRw8*, share the DRw52 specificity. The members of the DRw53 group, *DR4*, *DR7*, and *DRw9*, share a specificity referred to as DRw53 (Bodmer and Bodmer 1984). Together these haplotypes account for more than 80% of known DR specificities. The epitopes recognized by supertypic sera could be encoded by a single *DR $\beta$*  chain locus or by conserved regions shared by several  $\beta$  chain loci.

The identification of multiple *HLA-DR $\beta$*  chain loci (Long et al. 1983) and the possibility of nonequal rates of divergence of these loci led us to propose that a supertypic epitope could be encoded by a less polymorphic locus shared among several haplotypes (Gorski et al. 1985). Analysis of one of the *HLA-DR $\beta$*  chain genes expressed in DNA-transfected mouse fibroblasts has shown directly that it encodes the DRw52 specificity (Gorski et al. 1985). This gene has now been identified as the *DR $\beta$ III* locus of a

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*DRw52* haplotype (Rollini et al. 1985). In a *DRw53* haplotype, amino acid sequence analysis of the *DRw53* reactive product and the nucleotide sequence of genes cloned from a *DR4* haplotype have permitted the identification of one of the *DR<sub>β</sub>* chain loci as encoding *DRw53* (Sorrentino et al. 1985, Spies et al. 1985). It is generally assumed that *DRw52* and *DRw53* are encoded by alleles of the same locus (Bach 1985).

In this study, we have analyzed the structural relationship of the  $\beta$  chain genes of the DRw52 and DRw53 supertypic groups at the level of fine restriction maps and of DNA sequence. We can conclude that the two expressed *HLA-DR $\beta$*  chain loci in the DRw52 haplotypes (*DR $\beta$ I* and *DR $\beta$ III*) are homologous to the *DR $\beta$ I* locus of the DRw53 haplotypes, and that these three genes are presumably derived from a common ancestral locus, *DR $\beta$ I*. In contrast, the gene encoding the DRw53 specificity is distinct from these three genes and is most related to the *DR $\beta$ II* pseudogene of the DRw52 haplotypes. These two genes are presumably derived from another ancestral locus. The data suggest an evolutionary scheme for the *HLA-DR $\beta$*  chain region, where the genes encoding DRw52 and DRw53 are not alleles of the same ancestral locus. They also have practical implications concerning the nature and the magnitude of the structural differences among different *HLA-DR* alleles.

## Materials and Methods

**Isolation and nomenclature of DR $\beta$  chain genes.** The isolation and mapping of the DR $\beta$  chain genomic clones for the DR3 and DRw6 haplotypes have been described (Rollini et al. 1985). cDNA clones from a DR4, w6 cell line have also been published (Long et al. 1983). The DR4/DRw53 genomic clone was isolated from a phage library from the same DR4, w6 cell line. Four overlapping phage clones were isolated. The organization of the three DR $\beta$  chain genes has been described (Rollini et al. 1985). These loci are numbered in the direction of transcription using Roman numerals. The terms DRw52 supertypic group and DRw53 supertypic group are used to define the evolutionarily related groups of haplotypes sharing the DRw52 and DRw53 specificities, respectively. The terms DRw52 locus and DRw53 locus refer to the transcriptionally active locus which carries the DRw52 or DRw53 supertypic specificity and not the DR specificity. In DRw52, where the three DR $\beta$  loci have been linked, they are logically identified according to the gene order (DR $\beta$ I, DR $\beta$ II, DR $\beta$ III). In the case of DR4, however, all  $\beta$  chain loci have not yet been linked (Spies et al. 1985). and since four DR $\beta$  chain loci have been identified in certain DRw53 haplotypes (Böhme et al. 1985), the locus encoding DRw53 might in fact correspond to a DR $\beta$ IV locus (see Discussion).

**Oligonucleotide blot hybridization.** The oligonucleotides, 19mers, were kindly provided by Dr. E. Kawashima (Biogen S.A.) or synthesized using a Pharmacia Gene Assembler. The sequences which correspond to the different probes used are shown in Figure 1. The experimental protocol for the use of oligonucleotides under conditions of discrimination of single nucleotides is published (Angelini et al. 1986).

**Mapping of genomic clones.** The restriction enzyme maps presented here correspond to a fine level structural analysis of the genes. Mapping was performed by the classic single and double digestion techniques followed

by Southern blot analysis to localize the exons by hybridization with cDNA probes. Position of the exons is based on the maps of subclones used for sequencing the respective exons.

**Sequence analysis.** The DR3, DRw6a, and DRw6b first-domain sequences used for the sequence comparison are published elsewhere (Gorki and Mach 1986). The first domain sequences of the *DRw53* gene from a DR4 haplotype was determined from the genomic DR4 clone and from its corresponding cDNA (cDNA DR<sub>p</sub>IV in Long et al. 1983): The sequence for the DR4<sub>p</sub>I chain is from cDNA clone DR<sub>p</sub>II in Long et al. 1983 (B. Grubermann et al., unpublished data). The same sequences have been recently published from other DR4 cell lines (Spics et al. 1985, Gregersen et al. 1986a).

## Results

**Identification of the DRw53 locus by oligonucleotide Southern blot hybridization.** The DRw53 locus has been identified by comparison of partial amino acid sequence of a protein precipitated with anti-DRw53 sera with the DNA sequence of a gene from a DR4 haplotype (Sorrentino et al. 1985, Spies et al. 1985). We have determined the DNA sequence of the two expressed DR4 $\beta$  chain genes cloned from a DR4/w6 cell line and on the basis of these sequences, prepared oligonucleotide probes (4/1 and 4/2) which allow the unambiguous identification of one or the other locus (Fig. 1). The use of such 19 bp long oligonucleotides as probes to identify specific DR loci or specific DR alleles has been described in detail (Angelini et al. 1986). Probe 4/1 has been previously shown to hybridize only to DNA from DR4 individuals and thus identifies the corresponding sequence as that of the DR4 haplotypic locus (Angelini et al. 1986). In contrast, probe 4-2 hybridizes to DNA from cells of the DR4 and DR7 haplotypes, both members of the DRw53 supertypic group. Another pair of locus-specific probes (4/3 and 4/4) corresponding to another region of the first domain (see Fig. 1) showed identical results (data not shown). Therefore, the  $\beta$  chain gene from which the sequences of probes 4/2 and 4/4 were

FIRST DOMAIN SEQUENCE OF THE TWO EXPRESSED HLA-DQ  $\alpha$  CHAIN LOCUS  
IN A HLA DQ10 HAPLOTYPE

D81 X D F L E Q V K H E C M F F M G T Z R V F L  
 CAGCTTCTGCAGCAGGCTTAAACATCACTCTGATTCCTTCAAGCGGGBNBNBNCBCCCTCCCTCC  
 D84 X/93 CAGCTTCTGCAGCAGGCTTAAACATCACTCTGATTCCTTCAAGCGGGBNBNBNCBCCCTCCCTCCCT  
 L N N

D82 X D R Y V P V Q D P E Y U R P D S D V G E Y R D  
 GACGATATCTCTATCAACAGACACACATCCCTCCCTCCAGCGGAGCTCCGACATACCGCCGC  
 D14 X/93 ATCATATACATCTATCAACAGACACATCCCTCCCTCCAGCGGAGCTCCGACATACCGCCGC  
 I I N A Y N Q

D83 X V T E L G R D C T P A T C C C A C T Y M N A C C C A A C C C A A C C C T C A C C A C C  
 D84 X/93 CTCAACCACTCTCCCGCCCTCTGACCTGACTACTGCAACACCCAGAACCAACCTCTCTGACGACCC  
 A N

D84 X R A A V D T Y C C H N F A S D S B T V C C G  
 D81 X/93 CCCCCCAGCCGACACCACTCAACGACACCACTCCCTCCCTCCAGCTCAAGCTCTCAAGTCCGCG  
 CCCCCCAGCCGACACCTCAACGACACCACTCCCTCCCTCCAGCTCAAGCTCTCAAGTCCGCG

**Fig. 1.** First-domain sequence of DR4<sub>B</sub>I and DR4/DRw53. The region from which the oligonucleotide probes 4/1 and 4/2 are derived is underlined. The region corresponding to probes 4/3 and 4/4 is underlined twice.

J. Gorski et al

Structure 0:

DRUGS BIII

DAW6 BI

DR-53/MT:

DRUG BII

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Table I. Con

DR locus

DR4<sub>51</sub>  
DR4/DRw53

Results of comparisons with  
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## Structure of Loci Encoding HLA-DRw52 and w53

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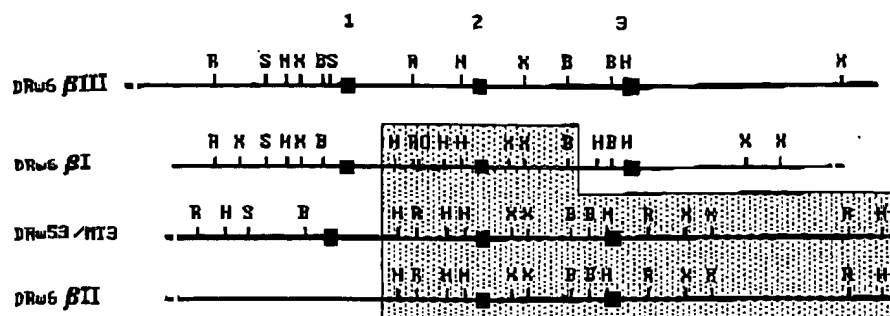


Fig. 2. Comparison of the maps of the three *DRw6* loci with the map of the *DR4/DRw53* locus. Sites for the following restriction enzymes are shown: B, Bam HI; H, Hind III; K, Xho I; R, Eco RI; S, Sac I; X, Xba. Regions of high homology are boxed. The black boxes refer to the exons encoding, respectively: 1, first domain; 2, second domain; 3, 3' UT

derived corresponds to the locus encoding the *DRw53* supertypic specificity.

The gene encoding the *DRw53* specificity is more related to the *DRβII* pseudogene than to any other *DRβ* genes of the *DRw52* haplotypes. In the *DRw52* haplotypes we have established a linkage map of three *DRβ* chain loci referred to as *DRβI*, *DRβII*, and *DRβIII* (Rollini et al. 1985). The *DRβI* and *DRβIII* loci are expressed whereas the *DRβII* locus lacks the first-domain exon and is thus considered a pseudogene (Rollini et al. 1985, 1987). Detailed restriction maps were generated for the three *DRw6β* chain loci.

A detailed map of the *DRw53* locus identified above was also prepared. It corresponds well to the map of the gene identified as *DRw53* on the basis of partial amino acid sequence (Sorrentino et al. 1985). This *DRw53* gene map was compared with maps of the three *DRβ* chain loci from the *DRw6* haplotype, *DRβI*, *DRβII*, and *DRβIII* (Fig. 2). As can be seen from the comparison, the best homology between the *DRw53* locus and any of the *DRw6* loci is between *DRw53* and *DRw6βII*. The homology between the two restriction maps extends well downstream of the exons encoding the protein itself and covers a region known to contain repetitive sequences. Similarity of noncoding regions of DNA, which are not likely to be under selective pressure, is indicative of an ancestral relationship.

The *DR4βI* locus is more related to the two expressed *DRw52* loci than it is to the locus encoding *DRw53*. The relationship between the genes of the *DRw52* and *DRw53* supertypic families was further analyzed by comparison of

nucleotide sequences. It had been shown earlier that *DR* polymorphism is mostly associated with the first domain of the polypeptide chain (Kaufman and Strominger 1982). The sequence of the first-domain exons of the *DR4βI* and *DR4-DRw53* loci are shown in Figure 1. These were compared with the first-domain exon sequences of the *DRβI* and *DRβIII* (*DRw52*) loci of the *DR3*, *DRw6a*, and *DRw6b* haplotypes, all members of the *DRw52* supertypic group. Table 1 shows the number of amino acid differences, with the numbers in parentheses corresponding to nucleotide differences. It is clear that the *DR4βI* locus is equally related to both the *DRβI* and *DRβIII* loci of haplotypes within the *DRw52* supertypic group and that it is more related to these loci than it is to the *DR4-DRw53* locus.

The distribution of allelic differences at locus *DRβI* and at the supertypic locus *DRβIII*. Comparison of DNA sequences from the first domain of *DRβ* chain genes also permits an analysis of the distribution of allelic differences. This analysis can shed light on which regions of the *DRβ* chain may be involved in contact with antigen and/or the T-cell receptor. It also indicates where polymorphic sites may influence recognition by serologic reagents. When all *DR* gene sequences are compared in a nonallelic manner and irrespective of supertypic boundaries, a pattern is seen (Figure 3A) where several major regions of sequence variability can be identified (bp 15-25; bp 65-100; bp 155-165; and bp 195-220). However, comparisons made at one given locus and within a supertypic family show a very different distribution of polymorphic sites. The simplest case is the series of *DR4* alleles at the *DRβI*

Table 1. Comparison of first domain sequences of *DRβ* chain genes

<i>DR</i> locus	<i>DRβI</i>	<i>DRw6aβI</i>	<i>DRw6bβI</i>	<i>DR3βIII</i> ( <i>DRw52a</i> )	<i>DRw6bβIII</i> ( <i>DRw52b</i> )	<i>DR4βI</i>
<i>DR4βI</i>	13 (22)	12 (21)	13 (22)	13 (21)	13 (20)	0
<i>DR4/DRw53</i>	23 (31)	22 (34)	20 (28)	24 (34)	21 (31)	18 (24)

Results of comparisons of first domain sequences of three haplotypes within the *DRw52* group with the *DRβI* and *DRw53* locus sequences. Allelic comparisons within the *DRw52* group are shown for *DRβI* (*DRw6a* and *b*) and for *DRβIII* (*DRw52a* and *b*). Numbers represent amino acid differences; numbers in parentheses indicate base pairs.

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Structure of

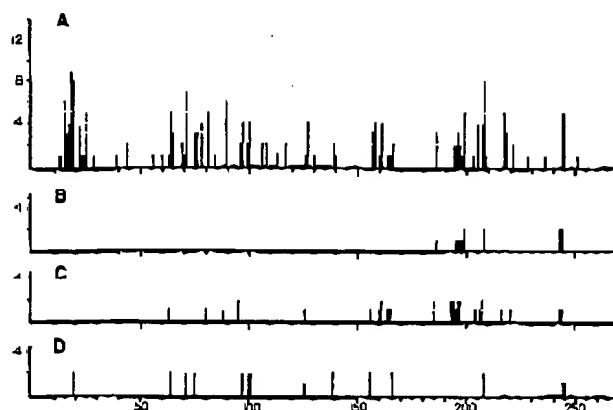


Fig. 3 A-D. Plot of distribution of polymorphic nucleotide sites in the first-domain encoding region. A Comparison of a number of *HLA-DR $\beta$*  chain genes irrespective of locus or supertypic group. The sequences used are from those presented here and those cited below as well as others previously published (Tonnelle et al. 1985, Gustafsson et al. 1984). B Comparison of alleles at the *DR $\beta$ 1* locus of a number of DR4 cell lines (Cairns et al. 1985, Gregersen et al. 1986a). C Comparison of alleles at the *DR $\beta$ 1* locus of a number of *DRw52* haplotypes (Gorski and Mach 1986, Tischer et al. 1986). D Comparison of alleles at the *DR $\beta$ 1* locus of a number of *DRw52* haplotypes (Gorski and Mach 1986, Didier et al. 1986). The height of the line indicates the frequency of the second most common nucleotide. An interrupted line indicates that more than two nucleotides are found at that position and the length of each part of the line corresponds to the frequency of one of the nucleotides

locus (Fig. 3B). These alleles are all recognized as DR4 by serology and are only distinguished by alloreactive T-cell reagents defining Dw specificities. As has been pointed out previously (Cairns et al. 1985, Gregersen et al. 1986a), these differences are found predominantly in the 185-210 bp region. When the alleles at the *DR $\beta$ 1* locus of

different haplotypes of the *DRw52* supertypic family are analyzed (Fig. 3C), the 185-210 bp region is also the most polymorphic segment, although some polymorphism is evident in the 155-165 bp region. In contrast and surprisingly, the alleles at the *DR $\beta$ 1* locus of the *DRw52* supertypic group show a very different distribution pattern from those observed at the *DR $\beta$ 1* locus of either the *DRw52* or *DRw53* supertypic group (Fig. 3D), with almost no variation in the 185-210 bp hypervariable segment.

The 15-25 bp region is only polymorphic when the comparison includes different loci and different supertypic groups (Fig. 3A). It is not polymorphic when alleles within a supertypic family are compared (Fig. 3B, C, and D). This indicates that the 15-25 bp region plays a role in distinguishing loci and supertypic groups rather than in restricted T-cell recognition.

### Discussion

The similarity of DR gene restriction maps in different haplotypes within an *HLA-DR* supertypic group and the concomitant differences across supertypic groups indicate that within such a supertypic group the different haplotypes are evolutionarily related. We have compared the structure of the different *DR $\beta$*  chain genes within and across supertypic groups in order to determine the relationship of the various loci to each other. Our first observation is that the gene encoding the *DRw53* specificity has characteristic structural features which correspond more closely to the *DR $\beta$ 1* pseudogene in the *DRw52* haplotypes than to any of the active *DR $\beta$*  chain loci, including the *DR $\beta$ 1* locus of the *DRw53* haplotypes. Comparison of first-domain se-

quences of *DR $\beta$*  either of *DR $\beta$*  than it is t

These *DRw52* loci these structures here in these two ancestral *DR $\beta$*  Figure 4, the *DRw52* *DR $\beta$ 1* locus the *DR $\beta$ 1* promoter two highly truncated *DR $\beta$*  (Rollini et al. 1986) organization of ancestral right). The early, and (Cairns et al. 1985) age is not been compared genes have (Böhme et al. 1986) should produce *DRw52* and to variation on the chromosome undergo alleles at locus mechanisms (1986).

This evolutionary data produced the *DR $\beta$*  ancestor and The *DR $\beta$ 1* *DRw52* family. More important each lineage thus the *DR $\beta$*  alleles in the *DR $\beta$*  In the *DR $\beta$*  *DR4* and *DR $\beta$*  and in their (Cairns et al. 1986a, less polymorphic been identified data). These into the 52a, oligonucleotide *DRw52b* allele

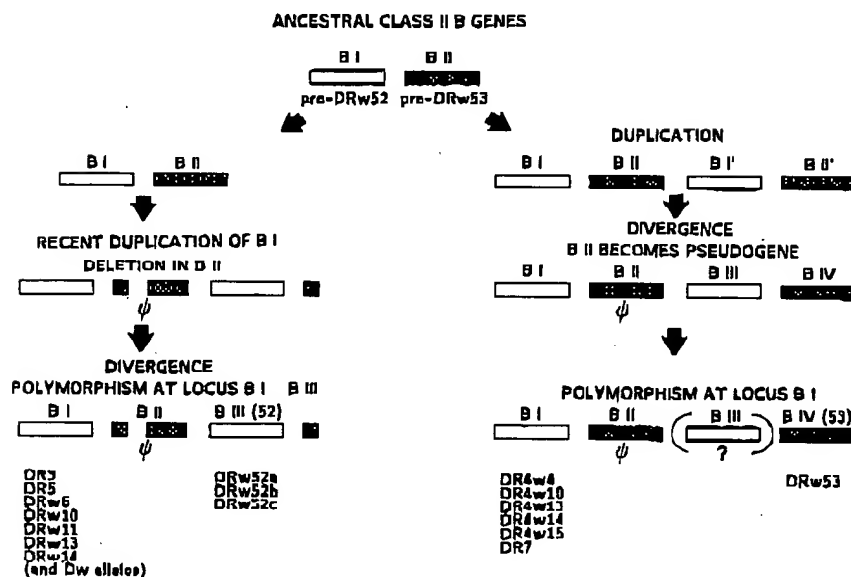


Fig. 4. Schematic representation of the evolutionary tree of the *DR $\beta$*  chain gene family. A two-locus family is postulated as the mammalian ancestral arrangement. The *DRw52* lineage (left) has undergone a deletion of most of the ancestral *DR $\beta$ 1* locus. The *DR $\beta$ 1* locus and promoter region of the *DR $\beta$ 1* locus were duplicated. These two events could have happened in opposite order or simultaneously. In the *DRw53* lineage the ancestral *DR $\beta$ 1-DR $\beta$ 1* pair was duplicated. Whether locus *DR $\beta$ 1* has been deleted or maintained will only be known when the linkage maps are available. Polymorphic variations were introduced at the *DR $\beta$ 1* locus at a higher rate than at the other loci, thus establishing haplotypic (*DR $\beta$ 1*) and supertypic (*DRw52* and *DRw53*) loci



quences of the active loci shows the corollary: the first locus of *DRw53* haplotype (*DR4p*) is more closely related to either of the two active *DRw52* loci (*DRpI* and *DRpIII*) than it is to the *DRw53* locus in its own haplotype.

These observations indicate that the *DRw53* and *DRw52* loci are not alleles in the classical sense. Based on these structural data, a limited evolutionary scheme is proposed here to explain the origin of HLA-DR polymorphism in these two supertypic groups (Fig. 4). We propose two ancestral *DRp* chain genes, *DRpI* (pre-*DRw52*) in white in Figure 4, and *DRpII* (pre-*DRw53*) in black in Figure 4. In the *DRw52* lineage (left), a deletion involved part of the *DRpII* locus and a duplication event took place involving the *DRpI* gene (in white in Fig. 4) and the remnant promoter region of the *DRpII* locus. This resulted in the two highly homologous *DRpI* and *DRpIII* genes and in the truncated *DRpII* pseudogene found in the *DRw52* lineage (Rollini et al. 1985). We postulate that the current *DRw53* organization arose by an early gene duplication of the pair of ancestral *DRp* chain loci resulting in four loci (Fig. 4, right). The ancestral *DRpII* locus became a pseudogene early, and has undergone extensive mutation (Larhammar et al. 1985). The fate of the third locus in the *DRw53* lineage is not yet known as the complete linkage map has not been completed (Spies et al. 1985). Since four *DRp* chain genes have been identified in certain *DRw53* haplotypes (Böhme et al. 1985), the *DRw53* locus (black in Fig. 4) should probably be referred to as *DRpIV*. In both the *DRw52* and *w53* lineages, the different loci were submitted to variable mutation rates depending on their position on the chromosome, with the locus adjacent to the *DRa* locus undergoing the least mutation. At this point, various alleles at locus *DRpI* (Fig. 4, bottom line) arose by different mechanisms, including gene conversion (Gorski and Mach 1986).

This evolutionary scheme accounts best for the structural data presented here. It implies that the *DRw53* locus and the *DRpII* locus of the *DRw52* family share a common ancestor and thus can be considered alleles (black boxes). The *DR4pI* locus and the *DRpI* and *DRpIII* loci of the *DRw52* family share a common ancestor (white boxes). More importantly, the origin of the supertypic locus in each lineage, *DRw52* and *DRw53*, is clearly different and thus the *DRw52* and *DRw53* loci cannot be considered alleles in the classical sense.

In the *DRw53* lineage, the *DRw53* locus is identical in *DR4* and *DR7* haplotypes which differ in their *DRpI* locus and in their Dw specificities (Cairns et al. 1985, Gregersen et al. 1986a, b). In the *DRw52* lineage, three alleles of the less polymorphic locus, *DRw52* or *DRpIII*, have recently been identified (Gorski and Mach 1986, and unpublished data). These alleles split the *DRw52* group of haplotypes into the S2a, b, and c subgroups. Segregation studies using oligonucleotide probes specific for the *DRw52a* and *DRw52b* alleles further indicate that the haplotypic DR and

Dw specificities are not encoded by the *DRpIII* locus but rather by the *DRpI* locus (Gorski et al. 1987).

The DNA sequence comparisons have allowed us to map the positions of allelic differences. When true allelic comparisons are made, within a supertypic group, the polymorphism of the *DRpI* locus is characterized by a "hypervariable region" corresponding to bp 185-210 (amino acids 67-77). It is of interest that this segment has been implicated as the site of micro-recombination/gene conversion events, which directly affect the specificity and restriction of T-cell recognition (Gorski and Mach 1986). Interestingly, allelic comparisons of the *DRpIII* locus in the *DRw52* supertypic group show a very different pattern of polymorphic sites, with little or no differences in the "hypervariable region" at bp 185-210. This suggests that the mechanisms responsible for the allelic polymorphism at locus *DRpI* and locus *DRpIII* are not the same. It also raises the question of the nature of T-cell recognition of the products of each of these loci and of whether these two DR products play similar or different roles in the immune response, in particular in restricted antigen presentation to T cells.

The differences in the structure of the two supertypic groups have major consequences for serological analysis. The *DRw53* locus does not have a corresponding allele in the *DRw52* family. Therefore, heterozygosity within and between supertypic groups does not imply the same degree of structural differences. For example, a DR3, DRw6a individual is really DR3, DRw6a, DRw52a whereas a DR3, DR4 individual is DR3, DR4, DRw52a, DRw53. This difference in relative heterozygosity may prove to have important implications in the ability to respond to a wider selection of antigens and in the association of HLA class II with disease susceptibility. More importantly, it indicates that in HLA matching for organ transplantation, all HLA-DR mismatches are not of identical magnitude and consequence, especially when the supertypic loci (*DRw52* and *DRw53*) are taken into account. As shown in the example above, a single DR mismatch within a supertypic group can imply only a minor difference limited to the *DRpI* gene product, whereas any mismatch across supertypic groups involves the additional differences in the DR antigen encoded in the *DRw52* and *DRw53* supertypic loci. We have therefore proposed (Mach et al. 1986) that in addition to the number of mismatches, the nature of the mismatch might have important practical consequences in transplantation and should be taken into consideration.

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## References

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